

## WEST Search History

DATE: Friday, February 25, 2005

<u>Hide?</u>	<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>
<i>DB=PGPB,USPT,EPAB; PLUR=YES; OP=ADJ</i>			
<input type="checkbox"/>	L30	l25 and l5	1
<input type="checkbox"/>	L29	l25 and l4	1
<input type="checkbox"/>	L28	L27 and l18	6
<input type="checkbox"/>	L27	L26 and l1	36
<input type="checkbox"/>	L26	l23 or l24	7864
<input type="checkbox"/>	L25	(ferrone or wang or hsu).in.	35918
<input type="checkbox"/>	L24	(424/184.1, 130.1)!/[CCLS]	0
<input type="checkbox"/>	L23	(530/300,327,328,387.1)!/[CCLS]	7864
<input type="checkbox"/>	L22	L2 and L18	1
<input type="checkbox"/>	L21	L20.clm.	3
<input type="checkbox"/>	L20	anti-gd3	86
<input type="checkbox"/>	L19	L18 and L15	46
<input type="checkbox"/>	L18	mimetic or peptidomimetic	21512
<input type="checkbox"/>	L17	GD3 with peptidomimetic	0
<input type="checkbox"/>	L16	GD3 with peptid\$	37
<input type="checkbox"/>	L15	gd3 with ganglioside	354
<input type="checkbox"/>	L14	gd3 ganglioside	130
<input type="checkbox"/>	L13	L12 and L11	39
<input type="checkbox"/>	L12	inhibit\$	572024
<input type="checkbox"/>	L11	L10 and L5	60
<input type="checkbox"/>	L10	L9 or L8	55343
<input type="checkbox"/>	L9	L6.clm.	36700
<input type="checkbox"/>	L8	L6.ab.	35568
<input type="checkbox"/>	L7	L6 and L5	77
<input type="checkbox"/>	L6	antibod\$	138401
<input type="checkbox"/>	L5	L4 or L3 or L2	94
<input type="checkbox"/>	L4	L1.clm.	62
<input type="checkbox"/>	L3	L1.ab.	39
<input type="checkbox"/>	L2	L1.ti.	14
<input type="checkbox"/>	L1	gd3	666

END OF SEARCH HISTORY

<b>Application Number</b>	<b>Application No.</b>	<b>Applicant(s)</b>
	10/618,336	FERRONE ET AL.
	Examiner	Art Unit
	Brandon J Fetterolf, PhD	1642

## **Protein Sequence Searches - February 2005**

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

Entrez
PubMed
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Search
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 for **#16 AND #5**
 Preview
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 Clear

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NLM Gateway

TOXNET

Consumer Health

Clinical Alerts

ClinicalTrials.gov

PubMed Central

#1 Search ishikawa Field: Author

#2 Search taki Field: Author

#3 Search #1 AND #2 Field: Author

#4 Search GD3 Field: Author

#5 Search GD3 Field: Title/Abstract

#6 Search #3 and #5 Field: Title/Abstract

#7 Search #3 Field: Title/Abstract, Limits: Publication Date to 1998

#8 Search mimetic Field: Title/Abstract, Limits: Publication Date to 2002

#9 Search #5 and #8 Field: Title/Abstract, Limits: Publication Date to 2002

#10 Search peptidomimetic Field: Title/Abstract, Limits: Publication Date to 2002

#11 Search #10 AND #5 Field: Title/Abstract, Limits: Publication Date to 2002

#12 Search mimetic Field: All Fields, Limits: Publication Date to 2002

#13 Search #12 ND #5 Limits: Publication Date to 2002

#14 Search willers Field: Author, Limits: Publication Date to 2002

#15 Search #14 AND #5 Field: Author, Limits: Publication Date to 2002

#16 Search #16 AND #5 Field: Author, Limits: Publication Date to 2002

#18 Search #16 AND #5 Field: Author, Limits: Publication Date to 2002

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# PubMed

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Entrez	PubMed	Nucleotide
Protein	Genome	Structure
Clipboard	OMIM	PMID
Preview	Go	Clear
PMC		
Journals		
Books		

### Field: Author, Limits: Publication Date to 2002

- Search History will be lost after eight hours of inactivity.
- To combine searches use # before search number, e.g., #2 AND #6.
- Search numbers may not be continuous; all searches are represented.
- Click on query # to add to strategy

### Search

### Most Recent Queries

Time Result

11:39:21 29

11:37:13 143

11:36:21 1

11:35:23 355

10:28:49 0

10:28:34 3142

10:28:21 0

10:28:09 553

10:27:38 0

10:27:27 3108

10:24:18 1809

10:24:08 0

10:23:56 49

10:23:48 1509

10:23:40 13940

http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?CMD=History&DB=pubmed

2/25/05

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[Department of Health & Human Services](#)

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Feb 23 2005 11:00:20

(FILE 'HOME' ENTERED AT 14:03:56 ON 25 FEB 2005)

FILE 'CANCERLIT' ENTERED AT 14:04:06 ON 25 FEB 2005

L1 641 S GD3  
L2 14360 S MIMIC? OR MIMETIC? OR PEPTIDOMIMETIC?  
L3 194977 S ANTIGEN?  
L4 8188 S IMMUNOGEN?  
L5 162627 S ANTIBOD?  
L6 82 S ANTI-GD3  
L7 20 S L1 AND L2  
L8 10 S L7 AND L4  
L9 10 S L8 AND L5  
L10 5 S L9 AND L3  
L11 5 S L10 NOT PY>2002

FILE 'MEDLINE' ENTERED AT 14:07:05 ON 25 FEB 2005

L12 1813 S GD3  
L13 63707 S MIMIC? OR MIMETIC? OR PEPTIDOMIMETIC?  
L14 595321 S ANTIGEN?  
L15 32569 S IMMUNOGEN?  
L16 680887 S ANTIBOD?  
L17 62 S L12 AND L13  
L18 26 S L17 AND L16  
L19 10 S L18 AND L15  
L20 6 S L19 NOT PY>2002

FILE 'CAPLUS' ENTERED AT 14:09:21 ON 25 FEB 2005

L21 6468 S GD3  
L22 0 S FERRONE/AU  
L23 64212 S MIMIC? OR MIMETIC? OR PEPTIDOMIMETIC?  
L24 357467 S ANTIGEN?  
L25 29966 S IMMUNOGEN?  
L26 426207 S ANTIBOD?  
L27 77 S L21 AND L23  
L28 29 S L27 AND L26  
L29 9 S L28 AND L25  
L30 6 S L29 AND (ANTI()GD3)

FILE 'PCTFULL' ENTERED AT 14:11:47 ON 25 FEB 2005

L31 600 S GD3  
L32 37018 S MIMIC? OR MIMETIC? OR PEPTIDOMIMETIC?  
L33 13 S L31/AB  
L34 107 S L31/CLM  
L35 34 S L31 (S) L32  
L36 14 S L35 AND L34  
L37 75273 S ANTIBOD?  
L38 3750 S L32/CLM  
L39 9 S L38 AND L36  
L40 0 S L39 AND L33  
L41 9 S L39 AND L37  
L42 4 S L41 NOT PY>2002

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OM protein - protein search, using sw model

Run on: February 23, 2005, 06:04:47 ; Search time 24 Seconds  
(without alignments)  
37.325 Million cell updates/sec

Title: US-10-618-336-6  
Perfect score: 70  
Sequence: 1 MCPTDMPASLCM 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
<hr/>						
1	41	58.6	90	4	US-09-358-383C-31	Sequence 31, Appl
2	41	58.6	960	4	US-09-694-777A-21	Sequence 21, Appl
3	41	58.6	962	4	US-09-614-480-9	Sequence 9, Appl
4	41	58.6	962	4	US-09-694-777A-3	Sequence 3, Appl
5	41	58.6	962	4	US-09-694-777A-24	Sequence 24, Appl
6	41	58.6	962	4	US-10-422-075-9	Sequence 9, Appl
7	41	58.6	987	4	US-09-694-777A-22	Sequence 22, Appl
8	41	58.6	988	4	US-09-614-480-2	Sequence 2, Appl
9	41	58.6	988	4	US-10-162-012-5	Sequence 5, Appl
10	41	58.6	988	4	US-10-162-012-12	Sequence 12, Appl
11	41	58.6	988	4	US-10-422-075-2	Sequence 2, Appl

12	41	58.6	989	4	US-09-694-777A-4	Sequence 4, Appli
13	41	58.6	989	4	US-09-694-777A-23	Sequence 23, Appli
14	40	57.1	96	4	US-09-403-343B-24	Sequence 24, Appli
15	39	55.7	166	4	US-09-252-991A-24322	Sequence 24322, A
16	38	54.3	103	4	US-09-252-991A-28978	Sequence 28978, A
17	38	54.3	2500	2	US-08-801-263A-2	Sequence 2, Appli
18	38	54.3	2500	3	US-09-102-248-2	Sequence 2, Appli
19	38	54.3	2500	4	US-09-367-764-2	Sequence 2, Appli
20	38	54.3	2517	2	US-08-801-263A-5	Sequence 5, Appli
21	38	54.3	2517	3	US-09-102-248-5	Sequence 5, Appli
22	38	54.3	2517	4	US-09-367-764-5	Sequence 5, Appli
23	37	52.9	250	4	US-09-270-767-61069	Sequence 61069, A
24	37	52.9	433	4	US-09-270-767-45556	Sequence 45556, A
25	37	52.9	534	4	US-09-270-767-46023	Sequence 46023, A
26	37	52.9	3830	4	US-09-693-205A-4	Sequence 4, Appli
27	36	51.4	42	4	US-09-270-767-31926	Sequence 31926, A
28	36	51.4	42	4	US-09-270-767-47143	Sequence 47143, A
29	36	51.4	200	4	US-09-252-991A-18742	Sequence 18742, A
30	36	51.4	256	4	US-09-949-016-7576	Sequence 7576, Ap
31	36	51.4	256	4	US-09-949-016-7577	Sequence 7577, Ap
32	36	51.4	280	4	US-09-949-016-9249	Sequence 9249, Ap
33	36	51.4	280	4	US-09-949-016-9250	Sequence 9250, Ap
34	36	51.4	306	4	US-09-270-767-41758	Sequence 41758, A
35	36	51.4	330	3	US-09-188-930-125	Sequence 125, App
36	36	51.4	330	4	US-09-312-283C-125	Sequence 125, App
37	36	51.4	404	3	US-09-191-608-18	Sequence 18, Appli
38	36	51.4	431	4	US-09-270-767-57907	Sequence 57907, A
39	36	51.4	443	4	US-09-266-965-131	Sequence 131, App
40	36	51.4	447	3	US-09-191-608-19	Sequence 19, Appli
41	36	51.4	471	3	US-09-191-608-17	Sequence 17, Appli
42	36	51.4	497	3	US-09-191-608-20	Sequence 20, Appli
43	36	51.4	555	4	US-09-270-767-42597	Sequence 42597, A
44	36	51.4	617	3	US-09-188-930-303	Sequence 303, App
45	36	51.4	617	4	US-09-312-283C-303	Sequence 303, App

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OM protein - protein search, using sw model

Run on: February 23, 2005, 06:37:08 ; Search time 354 Seconds  
 (without alignments)  
 11.093 Million cell updates/sec

Title: US-10-618-336-6  
 Perfect score: 70  
 Sequence: 1 MCPTDMPASLCM 12

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*

15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*

16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*

17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*

19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
					ID	
1	44	62.9	47	15	US-10-424-599-193456	Sequence 193456,
2	44	62.9	296	15	US-10-210-281-4	Sequence 4, Appli
3	44	62.9	307	15	US-10-210-281-6	Sequence 6, Appli
4	44	62.9	329	15	US-10-112-944-313	Sequence 313, App
5	44	62.9	351	15	US-10-333-572-3	Sequence 3, Appli
6	42	60.0	312	15	US-10-282-122A-51764	Sequence 51764, A
7	42	60.0	344	14	US-10-017-161-1954	Sequence 1954, Ap
8	42	60.0	344	15	US-10-292-798-1602	Sequence 1602, Ap
9	41	58.6	90	14	US-10-185-867-31	Sequence 31, Appli
10	41	58.6	263	16	US-10-437-963-164408	Sequence 164408,
11	41	58.6	648	16	US-10-322-696-33	Sequence 33, Appli
12	41	58.6	960	14	US-10-188-308-21	Sequence 21, Appli
13	41	58.6	960	14	US-10-188-296-21	Sequence 21, Appli
14	41	58.6	960	14	US-10-188-341-21	Sequence 21, Appli
15	41	58.6	960	14	US-10-188-297-21	Sequence 21, Appli
16	41	58.6	962	14	US-10-188-308-3	Sequence 3, Appli
17	41	58.6	962	14	US-10-188-308-24	Sequence 24, Appli
18	41	58.6	962	14	US-10-188-296-3	Sequence 3, Appli

19	41	58.6	962	14	US-10-188-296-24	Sequence 24, Appl
20	41	58.6	962	14	US-10-188-341-3	Sequence 3, Appli
21	41	58.6	962	14	US-10-188-341-24	Sequence 24, Appl
22	41	58.6	962	14	US-10-188-297-3	Sequence 3, Appli
23	41	58.6	962	14	US-10-188-297-24	Sequence 24, Appl
24	41	58.6	962	14	US-10-174-613-4	Sequence 4, Appli
25	41	58.6	962	14	US-10-174-613-5	Sequence 5, Appli
26	41	58.6	962	15	US-10-422-075-9	Sequence 9, Appli
27	41	58.6	987	14	US-10-188-308-22	Sequence 22, Appl
28	41	58.6	987	14	US-10-188-296-22	Sequence 22, Appl
29	41	58.6	987	14	US-10-188-341-22	Sequence 22, Appl
30	41	58.6	987	14	US-10-188-297-22	Sequence 22, Appl
31	41	58.6	988	10	US-09-875-321-5	Sequence 5, Appli
32	41	58.6	988	10	US-09-875-321-12	Sequence 12, Appl
33	41	58.6	988	14	US-10-128-323-2	Sequence 2, Appli
34	41	58.6	988	14	US-10-162-012-5	Sequence 5, Appli
35	41	58.6	988	14	US-10-162-012-12	Sequence 12, Appl
36	41	58.6	988	14	US-10-174-613-2	Sequence 2, Appli
37	41	58.6	988	14	US-10-174-613-3	Sequence 3, Appli
38	41	58.6	988	15	US-10-369-022-18	Sequence 18, Appl
39	41	58.6	988	15	US-10-422-075-2	Sequence 2, Appli
40	41	58.6	988	15	US-10-162-102-5	Sequence 5, Appli
41	41	58.6	988	15	US-10-162-102-12	Sequence 12, Appl
42	41	58.6	988	15	US-10-332-447-31	Sequence 31, Appl
43	41	58.6	988	16	US-10-322-696-36	Sequence 36, Appl
44	41	58.6	988	17	US-10-916-061-5	Sequence 5, Appli
45	41	58.6	988	17	US-10-916-061-12	Sequence 12, Appl

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 23, 2005, 06:41:39 ; Search time 129 Seconds  
 (without alignments)  
 152.212 Million cell updates/sec

Title: US-10-618-336-6  
 Perfect score: 70  
 Sequence: 1 MCPTDMPASLCM 12

Scoring table: BLOSUM62  
 Xgapop 10.0 , Xgapext 0.5  
 Ygapop 10.0 , Ygapext 0.5  
 Fgapop 6.0 , Fgapext 7.0  
 Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
 Listing first 45 summaries

Command line parameters:

```
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US10618336/runat_18022005_145631_15147/app_query.fasta_1.1
99
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10618336@CGN_1_1_177@runat_18022005_145631_15147 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEX=7
```

Database : Issued\_Patents\_NA:  
 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*
 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*
 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*
 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*
 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*
 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result		Query						Description
	No.	Score	Match	Length	DB	ID		
<hr/>								
c	1	51	72.9	601	4	US-09-949-016-67848		Sequence 67848, A
c	2	51	72.9	162841	4	US-09-949-016-13733		Sequence 13733, A
c	3	47	67.1	2487	4	US-09-573-080A-80		Sequence 80, Appl
c	4	47	67.1	86936	4	US-09-949-016-17314		Sequence 17314, A
	5	46	65.7	767677	4	US-09-949-016-12147		Sequence 12147, A
	6	46	65.7	767677	4	US-09-949-016-17361		Sequence 17361, A
	7	45	64.3	292	4	US-09-602-565-19		Sequence 19, Appl
	8	45	64.3	299	4	US-09-602-565-18		Sequence 18, Appl
	9	45	64.3	502	4	US-09-602-565-9		Sequence 9, Appli
	10	45	64.3	548	4	US-09-602-565-10		Sequence 10, Appl
	11	45	64.3	577	4	US-09-602-565-11		Sequence 11, Appl
	12	45	64.3	601	4	US-09-949-016-136449		Sequence 136449,
c	13	45	64.3	6063	1	US-08-195-744-4		Sequence 4, Appli
c	14	45	64.3	6063	2	US-08-788-279-4		Sequence 4, Appli
c	15	45	64.3	17488	4	US-09-949-016-15574		Sequence 15574, A
c	16	44	62.9	601	4	US-09-949-016-53650		Sequence 53650, A
c	17	44	62.9	601	4	US-09-949-016-140101		Sequence 140101,
	18	44	62.9	601	4	US-09-949-016-156494		Sequence 156494,
	19	44	62.9	7376	4	US-09-949-016-4052		Sequence 4052, Ap
	20	44	62.9	12225	4	US-09-949-016-17360		Sequence 17360, A
c	21	44	62.9	91538	4	US-09-949-016-15703		Sequence 15703, A
	22	44	62.9	123513	4	US-09-949-016-15794		Sequence 15794, A
c	23	44	62.9	160759	4	US-09-949-016-16514		Sequence 16514, A

C 24	44	62.9	231129	4	US-09-949-016-16110	Sequence 16110, A
25	44	62.9	250715	4	US-09-949-016-13294	Sequence 13294, A
C 26	44	62.9	266293	4	US-09-949-016-11934	Sequence 11934, A
27	44	62.9	536165	4	US-09-214-808-1	Sequence 1, Appli
28	44	62.9	678533	4	US-09-949-016-14577	Sequence 14577, A
29	44	62.9	678533	4	US-09-949-016-14578	Sequence 14578, A
30	43	61.4	695	5	PCT-US93-06251-21	Sequence 21, Appl
31	43	61.4	1188	4	US-09-270-767-12519	Sequence 12519, A
32	43	61.4	4810	3	US-09-596-824-5	Sequence 5, Appli
33	43	61.4	4810	4	US-09-885-329-5	Sequence 5, Appli
C 34	43	61.4	6158	4	US-09-919-497-6	Sequence 6, Appli
35	43	61.4	6453	1	US-08-306-691B-14	Sequence 14, Appl
36	43	61.4	6453	3	US-09-209-668-10	Sequence 10, Appl
37	43	61.4	6453	3	US-09-356-952-8	Sequence 8, Appli
C 38	43	61.4	45755	4	US-09-949-016-15889	Sequence 15889, A
39	43	61.4	47799	4	US-09-949-016-13363	Sequence 13363, A
40	43	61.4	64518	4	US-09-949-016-17289	Sequence 17289, A
41	43	61.4	194915	4	US-09-949-016-15584	Sequence 15584, A
42	42.5	60.7	601	4	US-09-949-016-21607	Sequence 21607, A
43	42.5	60.7	601	4	US-09-949-016-21608	Sequence 21608, A
44	42.5	60.7	601	4	US-09-949-016-142272	Sequence 142272,
45	42.5	60.7	601	4	US-09-949-016-142273	Sequence 142273,

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 23, 2005, 07:39:25 ; Search time 380 Seconds  
 (without alignments)  
 186.647 Million cell updates/sec

Title: US-10-618-336-6  
 Perfect score: 70  
 Sequence: 1 MCPTDMPASLCM 12

Scoring table: BLOSUM62  
 Xgapop 10.0 , Xgapext 0.5  
 Ygapop 10.0 , Ygapext 0.5  
 Fgapop 6.0 , Fgapext 7.0  
 Delop 6.0 , Delext 7.0

Searched: 5384158 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Command line parameters:  
 -MODEL=frame+\_p2n.model -DEV=xlh

```

Q=/cgn2_1/USPTO_spool/US10618336/runat_18022005_145632_15239/app_query.fasta_1.1
99
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10618336@CGN_1_1_678@runat_18022005_145632_15239
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
-----	-----	-----	-----	-----	-----	-----
1	53	75.7	790	17	US-10-012-697-38	Sequence 38, Appl
c 2	51	72.9	613	18	US-10-357-930-19541	Sequence 19541, A
c 3	51	72.9	658	18	US-10-357-930-49337	Sequence 49337, A
4	51	72.9	674	13	US-10-027-632-235370	Sequence 235370,
5	51	72.9	674	13	US-10-027-632-235371	Sequence 235371,
6	51	72.9	674	17	US-10-027-632-235370	Sequence 235370,
7	51	72.9	674	17	US-10-027-632-235371	Sequence 235371,
c 8	47	67.1	418	10	US-09-918-995-11767	Sequence 11767, A
c 9	47	67.1	2487	10	US-09-854-867-80	Sequence 80, Appl
10	46	65.7	940	15	US-10-017-161-1389	Sequence 1389, Ap
11	46	65.7	943	15	US-10-017-161-1385	Sequence 1385, Ap
c 12	46	65.7	979	9	US-09-925-300-690	Sequence 690, App

13	46	65.7	13654	17	US-10-292-798-1131	Sequence 1131, Ap
14	46	65.7	47804	15	US-10-017-161-717	Sequence 717, App
15	46	65.7	47804	17	US-10-292-798-629	Sequence 629, App
c 16	45	64.3	290	18	US-10-425-115-34478	Sequence 34478, A
17	45	64.3	299	15	US-10-280-953-13	Sequence 13, Appl
18	45	64.3	300	18	US-10-425-115-156755	Sequence 156755,
19	45	64.3	362	18	US-10-767-701-22224	Sequence 22224, A
20	45	64.3	502	15	US-10-280-953-9	Sequence 9, Appli
c 21	45	64.3	520	16	US-10-029-386-1283	Sequence 1283, Ap
22	45	64.3	671	18	US-10-767-701-6366	Sequence 6366, Ap
c 23	45	64.3	702	15	US-10-156-761-7433	Sequence 7433, Ap
c 24	45	64.3	752	18	US-10-425-115-28784	Sequence 28784, A
25	45	64.3	871	18	US-10-425-115-174480	Sequence 174480,
c 26	45	64.3	27007	9	US-09-764-868-1424	Sequence 1424, Ap
c 27	45	64.3	31477	13	US-10-087-192-373	Sequence 373, App
c 28	45	64.3	155937	18	US-10-723-860-2208	Sequence 2208, Ap
29	45	64.3	158405	14	US-10-175-523-86	Sequence 86, Appl
30	45	64.3	9025608	15	US-10-156-761-1	Sequence 1, Appli
c 31	44	62.9	142	17	US-10-424-599-50614	Sequence 50614, A
c 32	44	62.9	350	18	US-10-357-930-14433	Sequence 14433, A
c 33	44	62.9	386	18	US-10-357-930-35543	Sequence 35543, A
c 34	44	62.9	386	18	US-10-357-930-44355	Sequence 44355, A
c 35	44	62.9	390	17	US-10-424-599-2370	Sequence 2370, Ap
36	44	62.9	543	10	US-09-764-891-1368	Sequence 1368, Ap
37	44	62.9	543	10	US-09-764-891-7744	Sequence 7744, Ap
c 38	44	62.9	600	13	US-10-027-632-141934	Sequence 141934,
c 39	44	62.9	600	13	US-10-027-632-141935	Sequence 141935,
c 40	44	62.9	600	13	US-10-027-632-141936	Sequence 141936,
c 41	44	62.9	600	17	US-10-027-632-141934	Sequence 141934,
c 42	44	62.9	600	17	US-10-027-632-141935	Sequence 141935,
c 43	44	62.9	600	17	US-10-027-632-141936	Sequence 141936,
c 44	44	62.9	605	18	US-10-021-323-1034	Sequence 1034, Ap
c 45	44	62.9	888	14	US-10-198-846-3405	Sequence 3405, Ap

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OM protein - protein search, using sw model

Run on: February 23, 2005, 04:36:07 ; Search time 74 Seconds  
(without alignments)  
62.718 Million cell updates/sec

Title: US-10-618-336-6

Perfect score: 70

Sequence: 1 MCPTDMPASLCM 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result No.	Query					Description
	Score	Match	Length	DB	ID	
<hr/>						
1	44	62.9	121	4	AAB95737	Aab95737 Human pro
2	44	62.9	296	8	ADJ50939	Adj50939 Human nov
3	44	62.9	307	8	ADJ50941	Adj50941 Human nov
4	44	62.9	329	8	ADM87220	Adm87220 Human pro
5	44	62.9	351	5	AAE18955	Aae18955 Human cel
6	44	62.9	351	8	ADN01129	Adn01129 Human cel
7	42	60.0	262	3	AAG43457	Aag43457 Arabidops
8	42	60.0	262	3	AAG23843	Aag23843 Arabidops
9	42	60.0	312	6	ABU23840	Abu23840 Protein e

10	42	60.0	344	7	ADC87149	Adc87149 Human GPC
11	42	60.0	351	3	AAG23842	Aag23842 Arabidops
12	42	60.0	351	3	AAG43456	Aag43456 Arabidops
13	42	60.0	381	3	AAG43455	Aag43455 Arabidops
14	42	60.0	381	3	AAG23841	Aag23841 Arabidops
15	41	58.6	90	6	ABU61687	Abu61687 Program d
16	41	58.6	90	7	ADB66818	Adb66818 Potassium
17	41	58.6	348	1	AAP94682	Aap94682 Human man
18	41	58.6	648	8	ADQ59397	Adq59397 Human can
19	41	58.6	856	7	ABW01409	Abw01409 Human HEA
20	41	58.6	962	3	AAY49944	Aay49944 Human pot
21	41	58.6	988	4	AAB31714	Aab31714 A human a
22	41	58.6	988	4	AAE01043	Aae01043 Human eth
23	41	58.6	988	5	ABG70999	Abg70999 Human tra
24	41	58.6	988	5	ABB76165	Abb76165 Human pot
25	41	58.6	988	5	AAO14214	Aao14214 Human tra
26	41	58.6	988	7	ADC77655	Adc77655 Human 334
27	41	58.6	988	7	ABW01364	Abw01364 Human pot
28	41	58.6	988	8	ADQ59400	Adq59400 Human can
29	41	58.6	989	3	AAY49945	Aay49945 Human pot
30	41	58.6	989	7	ADC77667	Adc77667 Human 332
31	41	58.6	989	8	ADR44914	Adr44914 Polypepti
32	41	58.6	1174	4	ABB65304	Abb65304 Drosophil
33	40	57.1	59	8	ABO56119	Abo56119 Human gen
34	40	57.1	84	4	AAU63085	Aau63085 Propionib
35	40	57.1	84	6	ABM59604	Abm59604 Propionib
36	40	57.1	699	8	ABO84631	Abo84631 Mouse can
37	40	57.1	1178	8	ADP74025	Adp74025 Murine CD
38	39	55.7	85	4	AAU21335	Aau21335 Human nov
39	39	55.7	103	4	AAU59241	Aau59241 Propionib
40	39	55.7	103	6	ABM55760	Abm55760 Propionib
41	39	55.7	166	7	ABO75576	Abo75576 Pseudomon
42	39	55.7	194	3	AAG61086	Aag61086 Arabidops
43	39	55.7	194	3	AAG56099	Aag56099 Arabidops
44	39	55.7	198	3	AAG56098	Aag56098 Arabidops
45	39	55.7	198	3	AAG61085	Aag61085 Arabidops

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 23, 2005, 06:38:09 ; Search time 2602 Seconds  
 (without alignments)  
 223.468 Million cell updates/sec

Title: US-10-618-336-6  
 Perfect score: 70  
 Sequence: 1 MCPTDMPASLCM 12

Scoring table: BLOSUM62  
 Xgapop 10.0 , Xgapext 0.5  
 Ygapop 10.0 , Ygapext 0.5  
 Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh  
-  
Q=/cgn2\_1/USPTO\_spool/US10618336/runat\_18022005\_145630\_15121/app\_query.fasta\_1.1  
99  
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10618336@CGN\_1\_1\_4200@runat\_18022005\_145630\_15121 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:  
1: gb\_ba:  
2: gb\_htg:  
3: gb\_in:  
4: gb\_om:  
5: gb\_ov:  
6: gb\_pat:  
7: gb\_ph:  
8: gb\_pl:  
9: gb\_pr:  
10: gb\_ro:  
11: gb\_sts:  
12: gb\_sy:  
13: gb\_un:  
14: gb\_vi:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result	Query					Description
	No.	Score	Match	Length	DB	
ID						
c	1	54	77.1	10465	1	AE008241 Agrobacte
	2	54	77.1	13358	1	AE009373 Agrobacte
	3	53	75.7	864	6	AX540791 Sequence
	4	53	75.7	35447	2	AC007181 Homo sapi
	5	53	75.7	39972	2	AC087250 Homo sapi

c	6	53	75.7	146534	9	AC092143	AC092143 Homo sapi
c	7	53	75.7	193729	4	AC129099	AC129099 Canis fam
c	8	53	75.7	202454	2	AC128934	AC128934 Rattus no
c	9	53	75.7	210446	9	AC133919	AC133919 Homo sapi
	10	53	75.7	235804	2	AC106639	AC106639 Rattus no
c	11	53	75.7	261914	2	AC122581	AC122581 Rattus no
	12	53	75.7	348283	2	AC125706	AC125706 Rattus no
c	13	52	74.3	193041	10	AC110169	AC110169 Mus muscu
	14	52	74.3	277112	2	AC131428	AC131428 Rattus no
c	15	51	72.9	613	6	CQ487674	CQ487674 Sequence
	16	51	72.9	616	11	BV053434	BV053434 S212P6035
c	17	51	72.9	658	6	CQ517470	CQ517470 Sequence
	18	51	72.9	97101	2	AL450308	AL450308 Homo sapi
	19	51	72.9	106341	9	AL390316	AL390316 Human DNA
c	20	51	72.9	130878	9	AL450063	AL450063 Human DNA
	21	51	72.9	164485	2	AC025340	AC025340 Homo sapi
c	22	51	72.9	167218	2	AC069041	AC069041 Homo sapi
	23	51	72.9	176161	2	AC021173	AC021173 Homo sapi
	24	51	72.9	185953	10	AC123872	AC123872 Mus muscu
	25	51	72.9	215326	9	AC091160	AC091160 Homo sapi
	26	51	72.9	216400	2	AC125934	AC125934 Rattus no
c	27	51	72.9	216601	2	AC129691	AC129691 Rattus no
c	28	51	72.9	218618	10	AL928587	AL928587 Mouse DNA
	29	51	72.9	237855	2	AC136663	AC136663 Rattus no
	30	51	72.9	244238	2	AC131627	AC131627 Rattus no
	31	51	72.9	250663	2	AC134905	AC134905 Mus muscu
c	32	51	72.9	258792	2	AC135491	AC135491 Rattus no
	33	50	71.4	39089	4	AF483210	AF483210 Canis fam
	34	50	71.4	110000	2	AC096220_1	Continuation (2 of
c	35	50	71.4	212129	2	AC139817	AC139817 Homo sapi
	36	50	71.4	219683	2	AC103126	AC103126 Rattus no
	37	50	71.4	222587	2	AC109744	AC109744 Rattus no
	38	50	71.4	242510	2	AC128507	AC128507 Rattus no
c	39	49	70.0	110000	2	AC091343_0	AC091343 Rattus no
c	40	49	70.0	148965	2	AC136069	AC136069 Rattus no
c	41	49	70.0	151881	9	AC008629	AC008629 Homo sapi
c	42	49	70.0	171011	10	AC140244	AC140244 Mus muscu
c	43	49	70.0	174203	2	AC141570	AC141570 Rattus no
c	44	49	70.0	174640	2	AC017044	AC017044 Homo sapi
c	45	49	70.0	176427	2	AC151671	AC151671 Gallus ga

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 23, 2005, 06:37:39 ; Search time 361 Seconds  
 (without alignments)  
 196.778 Million cell updates/sec

Title: US-10-618-336-6  
 Perfect score: 70  
 Sequence: 1 MCPTDMPASLCM 12

Scoring table: BLOSUM62  
 Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

-Q=/cgn2\_1/USPTO\_spool/US10618336/runat\_18022005\_145629\_15113/app\_query.fasta\_1.1  
99  
-DB=N\_Geneseq\_16Dec04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10618336\_@CGN\_1\_1\_644\_@runat\_18022005\_145629\_15113 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_16Dec04:  
1: geneseqn1980s:  
2: geneseqn1990s:  
3: geneseqn2000s:  
4: geneseqn2001as:  
5: geneseqn2001bs:  
6: geneseqn2002as:  
7: geneseqn2002bs:  
8: geneseqn2003as:  
9: geneseqn2003bs:  
10: geneseqn2003cs:  
11: geneseqn2003ds:  
12: geneseqn2004as:  
13: geneseqn2004bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
	1	53	75.7	790	9	ADB81726 Human cDN
	2	53	75.7	864	6	Abq88782 Human pro
c	3	51	72.9	613	5	Abv19550 Human pro
c	4	51	72.9	658	5	Abv49318 Human pro

c	5	47	67.1	418	9	ACH24555	Ach24555 Human adu
c	6	47	67.1	2487	7	ADS31047	Ads31047 Human gen
c	7	46	65.7	303	6	AAS98123	Aas98123 Human DNA
c	8	46	65.7	979	3	AAF16255	Aaf16255 Human pro
c	9	46	65.7	1215	13	ADR85721	Adr85721 Aspergill
c	10	46	65.7	1326	13	ADR85134	Adr85134 Aspergill
c	11	46	65.7	7326	13	ADR84547	Adr84547 Aspergill
	12	46	65.7	13654	10	ADC86678	Adc86678 Human GPC
	13	46	65.7	47804	10	ADC86176	Adc86176 Human GPC
	14	45	64.3	292	8	ABX94157	Abx94157 Incyte ID
	15	45	64.3	299	8	ABX94156	Abx94156 Incyte ID
	16	45	64.3	299	10	AAD61596	Aad61596 Rat MAPOP
c	17	45	64.3	478	4	AAI85737	Aai85737 Human pol
	18	45	64.3	502	8	ABX94147	Abx94147 Incyte ID
	19	45	64.3	502	10	AAD61592	Aad61592 Rat MAPOP
c	20	45	64.3	520	12	ACH68088	Ach68088 Human gen
	21	45	64.3	548	8	ABX94148	Abx94148 Incyte ID
	22	45	64.3	577	8	ABX94149	Abx94149 Incyte ID
	23	45	64.3	586	4	AAK63266	Aak63266 Human imm
c	24	45	64.3	6063	2	AAQ37205	Aaq37205 Delta-ami
c	25	45	64.3	27007	4	AAS27764	Aas27764 DNA encod
c	26	45	64.3	27007	10	ADB94567	Adb94567 Novel hum
c	27	45	64.3	31477	11	ACN44096	Acn44096 Mouse gen
c	28	45	64.3	90400	12	ADP08389	Adp08389 Human chr
c	29	45	64.3	155937	12	ADQ19389	Adq19389 Human sof
c	30	44	62.9	350	5	ABV14442	Abv14442 Human pro
c	31	44	62.9	386	5	ABV35525	Abv35525 Human pro
c	32	44	62.9	386	5	ABV44336	Abv44336 Human pro
c	33	44	62.9	457	4	AAL12073	Aal12073 Human bre
	34	44	62.9	543	4	AAL01367	Aal01367 Human rep
	35	44	62.9	543	4	AAL05056	Aal05056 Human rep
	36	44	62.9	543	4	ABL97949	Ab197949 Human tes
	37	44	62.9	543	4	ABL96820	Ab196820 Human tes
c	38	44	62.9	605	13	ACN46253	Acn46253 Cotton pr
	39	44	62.9	607	13	ADQ52289	Adq52289 Novel can
	40	44	62.9	794	4	AAH05678	Aah05678 Human cDN
c	41	44	62.9	888	11	ACN82255	Acn82255 Breast ca
	42	44	62.9	1015	12	ADJ50940	Adj50940 Human cDN
	43	44	62.9	1188	12	ADJ50938	Adj50938 Human cDN
c	44	44	62.9	1242	4	ABL25337	Ab125337 Drosophil
	45	44	62.9	1566	10	ADE07579	Ade07579 Novel cod

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OM protein - protein search, using sw model

Run on: February 23, 2005, 06:02:22 ; Search time 23 Seconds  
 (without alignments)  
 50.200 Million cell updates/sec

Title: US-10-618-336-6  
 Perfect score: 70  
 Sequence: 1 MCPTDMPASLCM 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	47	67.1	3839	2	T49799	related to TOM1 pr
2	42	60.0	312	2	G97162	hypothetical prote
3	42	60.0	381	2	F84615	hypothetical prote
4	42	60.0	1206	2	E86445	hypothetical prote
5	41	58.6	763	2	A47563	glucose-6-phosphat
6	41	58.6	934	2	T42394	potassium channel
7	41	58.6	962	2	I53197	potassium channel
8	41	58.6	989	2	I48912	potassium channel
9	41	58.6	1174	2	A40853	potassium channel
10	40	57.1	471	2	AC2014	two-component sens
11	40	57.1	1178	2	S44142	VLA-2 protein homo
12	39	55.7	537	2	I51592	protein-tyrosine k
13	38.5	55.0	172	2	T34413	hypothetical prote
14	38	54.3	320	2	T09288	late embryonic abu
15	38	54.3	746	2	T43648	probable sexual cy
16	38	54.3	1461	2	T13157	mitotic checkpoint
17	37	52.9	182	2	D70859	hypothetical prote
18	37	52.9	388	2	T06035	hypothetical prote
19	37	52.9	398	1	TVFVVR	transforming prote
20	37	52.9	676	2	A45984	sperm-binding glyc
21	37	52.9	782	2	T22134	hypothetical prote
22	36.5	52.1	965	2	T12545	hypothetical prote
23	36	51.4	130	2	G86804	cytidine deaminase
24	36	51.4	249	2	H71131	hypothetical prote
25	36	51.4	384	2	AG3494	recF protein [impo
26	36	51.4	408	2	S33683	site-specific DNA-
27	36	51.4	1611	2	T38236	hypothetical prote

28	36	51.4	1894	2	JC4980	plexin 1 precursor
29	36	51.4	2533	2	T28675	alpha-51D immobili
30	36	51.4	2533	2	T28674	alpha-51D-immobili
31	35.5	50.7	561	2	T11378	NADH2 dehydrogenas
32	35	50.0	131	2	AG3198	hypothetical prote
33	35	50.0	138	2	T48293	hypothetical prote
34	35	50.0	220	2	T30688	hypothetical prote
35	35	50.0	237	2	T24407	hypothetical prote
36	35	50.0	246	2	S74408	lipopeptide antibi
37	35	50.0	321	2	E97741	D-alanine-D-alanin
38	35	50.0	360	2	T35783	probable secreted
39	35	50.0	365	2	T43286	cet-1 protein - Ca
40	35	50.0	377	2	AD2922	altronate oxidored
41	35	50.0	377	2	E97696	altronate oxidored
42	35	50.0	379	2	T29518	hypothetical prote
43	35	50.0	432	2	T23762	hypothetical prote
44	35	50.0	461	2	T41369	hypothetical prote
45	35	50.0	466	2	F69331	conserved hypothet

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 23, 2005, 06:41:19 ; Search time 2133 Seconds  
 (without alignments)  
 214.145 Million cell updates/sec

Title: US-10-618-336-6  
 Perfect score: 70  
 Sequence: 1 MCPTDMPASLCM 12

Scoring table: BLOSUM62  
 Xgapop 10.0 , Xgapext 0.5  
 Ygapop 10.0 , Ygapext 0.5  
 Fgapop 6.0 , Fgapext 7.0  
 Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Command line parameters:  
 -MODEL=frame+\_p2n.model -DEV=xlh

Q=/cgn2\_1/USPTO\_spool/US10618336/runat\_18022005\_145630\_15135/app\_query.fasta\_1.1  
 99  
 -DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45

```

-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10618336 @CGN_1_1_4352 @runat_18022005_145630_15135 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

```

Database : EST:\*

```

1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
	1	53	75.7	838	8	BZ200466 CH230-445
c	2	53	75.7	1721	3	BC045753 Homo sapi
	3	52	74.3	560	8	BZ109194 CH230-158
	4	51	72.9	753	4	BI116555 602868601
	5	50	71.4	713	9	CG132573 PUIIS63TB
c	6	50	71.4	868	9	CG100176 PUFSZ03TB
	7	50	71.4	873	9	CG100178 PUFSZ03TD
c	8	50	71.4	945	8	CC195750 ZMMBBC031
	9	49	70.0	175	9	CE305331 tigr-gss-
c	10	49	70.0	290	8	BZ857894 CH240_206
	11	49	70.0	396	6	CB773497 AMGNNUC:N
	12	49	70.0	408	8	BH110778 RPCI-24-3
	13	49	70.0	513	8	BZ300561 KD0792.R1
	14	49	70.0	607	9	CR177418 Reverse s
	15	49	70.0	705	9	AG301037 Mus muscu
	16	49	70.0	724	9	AG119495 Pan trogl
	17	49	70.0	736	9	AG565506 Mus muscu
	18	49	70.0	759	8	AZ254101 RPCI-23-6
	19	49	70.0	1013	5	BU262687 603820370
	20	49	70.0	2320	3	BC036311 Homo sapi
c	21	48	68.6	397	1	AI023232 ov78e02.s
c	22	48	68.6	480	8	BZ408900 OGABS66TM
	23	48	68.6	493	8	BZ408892 OGABS66TC
c	24	48	68.6	514	2	BF261235 1M0003B06
c	25	48	68.6	659	2	BE973830 601680637
c	26	48	68.6	770	9	CE024478 tigr-gss-
c	27	48	68.6	785	8	AZ046018 nbeb0088J
c	28	48	68.6	881	4	BI099923 602885050
	29	48	68.6	1040	4	BM466654 AGENCOURT
c	30	47	67.1	264	2	AW428085 64905 MAR

c 31	47	67.1	277	1	AT003318	AT003318 AT003318
c 32	47	67.1	282	9	CG943500	CG943500 MBEAX54TR
c 33	47	67.1	406	8	AZ650391	AZ650391 1M0520J01
34	47	67.1	408	5	BP938592	BP938592 25-026-P1
35	47	67.1	460	8	AZ015845	AZ015845 RPCI-23-3
c 36	47	67.1	469	4	BI680462	BI680462 458735 MA
37	47	67.1	508	8	AZ075000	AZ075000 RPCI-23-4
c 38	47	67.1	529	6	CA290583	CA290583 SCUTSD102
39	47	67.1	571	5	BU108507	BU108507 603110129
40	47	67.1	586	5	BQ556552	BQ556552 H4040G08-
c 41	47	67.1	662	4	BI078115	BI078115 602872423
c 42	47	67.1	712	9	CNS01TAE	AL166271 Tetraodon
43	47	67.1	718	7	CN839615	CN839615 AGENCOURT
44	47	67.1	728	5	BP437710	BP437710 BP437710
c 45	47	67.1	745	6	CD854754	CD854754 DH0AMM34Z

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OM protein - protein search, using sw model

Run on: February 23, 2005, 05:23:53 ; Search time 77 Seconds  
 (without alignments)  
 79.805 Million cell updates/sec

Title: US-10-618-336-6  
 Perfect score: 70  
 Sequence: 1 MCPTDMPASLCM 12

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : UniProt\_03:\*

- 1: uniprot\_sprot:\*
- 2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

\$

Result	Query				
No.	Score	Match	Length	DB	ID
-----					

1	47	67.1	4065	1	TOM1_NEUCR	Q9p4z1 neurospora
2	44	62.9	121	2	Q9H7W8	Q9h7w8 homo sapien
3	44	62.9	365	2	Q8IV13	Q8iv13 homo sapien
4	42	60.0	312	1	MRAW_CLOAB	Q97h81 clostridium
5	42	60.0	381	2	Q8LA81	Q8la81 arabidopsis
6	42	60.0	381	2	Q9ZQ45	Q9zq45 arabidopsis
7	42	60.0	1206	2	Q9FVQ7	Q9fvq7 arabidopsis
8	41	58.6	27	2	Q81172	Q81172 hepatitis b
9	41	58.6	204	2	Q986U1	Q986u1 rhizobium l
10	41	58.6	278	2	Q6Z2H6	Q6z2h6 oryza sativ
11	41	58.6	297	2	Q7QNM1	Q7qnm1 anopheles g
12	41	58.6	543	2	Q9W645	Q9w645 gallus gall
13	41	58.6	568	2	Q847W2	Q847w2 vibrio para
14	41	58.6	599	2	Q87PX3	Q87px3 vibrio para
15	41	58.6	763	1	G6PE_RABIT	P56201 oryctolagus
16	41	58.6	956	2	O44164	O44164 caenorhabdi
17	41	58.6	956	2	Q9XYX7	Q9xyx7 caenorhabdi
18	41	58.6	962	1	KCH1_RAT	Q63472 rattus norv
19	41	58.6	987	1	KCH1_BOVIN	O18965 bos taurus
20	41	58.6	988	1	KCH5_HUMAN	Q8ncm2 homo sapien
21	41	58.6	988	1	KCH5_RAT	Q9epi9 rattus norv
22	41	58.6	988	2	Q6NZH0	Q6nzh0 mus musculu
23	41	58.6	988	2	Q8C035	Q8c035 mus musculu
24	41	58.6	989	1	KCH1_HUMAN	Q95259 homo sapien
25	41	58.6	989	1	KCH1_MOUSE	Q60603 mus musculu
26	41	58.6	1007	2	Q7QCM9	Q7qcm9 anopheles g
27	41	58.6	1011	2	Q7YW98	Q7yw98 manduca sex
28	41	58.6	1174	1	CIKE_DROME	Q02280 drosophila
29	41	58.6	1174	2	Q9VXZ6	Q9vxz6 drosophila
30	41	58.6	1285	2	Q8JUV1	Q8juv1 avian reovi
31	40	57.1	323	2	Q8CB84	Q8cb84 mus musculu
32	40	57.1	471	2	Q8YWE8	Q8ywe8 anabaena sp
33	40	57.1	508	1	VL1 HPV60	P50821 human papil
34	40	57.1	1178	1	ITA2_MOUSE	Q62469 mus musculu
35	40	57.1	1178	2	Q6P1C7	Q6p1c7 mus musculu
36	40	57.1	2116	2	Q6D9Y1	Q6d9y1 erwinia car
37	40	57.1	2168	2	Q6LGA3	Q6lga3 photobacter
38	39	55.7	196	2	Q6Y2V5	Q6y2v5 desulfuromo
39	39	55.7	198	2	Q8LF87	Q8lf87 arabidopsis
40	39	55.7	222	2	Q9LT60	Q9lt60 arabidopsis
41	39	55.7	264	2	Q66IP2	Q66ip2 xenopus lae
42	39	55.7	300	2	Q9YUQ5	Q9yuq5 turkey aden
43	39	55.7	318	2	Q67Q57	Q67q57 symbiobacte
44	39	55.7	328	2	Q8LJD0	Q8ljd0 oryza sativ
45	39	55.7	346	2	Q652V2	Q652v2 oryza sativ